## SEQUENCE LISTING

<110> KYOWA HAKKO KOGYO CO., LTD

<120> Humanized anti-GD3 antibody and it's cytokine conjugate

<130>11239WO1

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<150>H11-278291

<151>1999-09-30

<160> 57

<170> PatentIn Ver. 2.0

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Ser His Tyr Ala Met Ser Trp Val Arg Gln Thr Pro Ala Lys Arg Leu 30 35 40 45

Glu Trp Val Ala Tyr Ile Ser Ser Gly Gly Ser Gly Thr Tyr Tyr Ser 50 55 60

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn 65 70 75

Thr Leu Tyr Leu Gln Met Arg Ser Leu Arg Ser Glu Asp Ser Ala Met 80 85 90

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Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Ser Ala Ser Gln Asp
Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val
Lys Leu Leu Ile Phe Tyr Ser Ser Asn Leu His Ser Gly Val Pro Ser
Arg Phe Ser Gly Gly Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser
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Ala Tyr Ile Ser Ser Gly Gly Ser Gly Thr Tyr Tyr Ser Asp Ser Val
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Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
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ggt acc aga tgt gac atc cag atg acc cag act gca tcc tcc ctg cct
Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Thr Ala Ser Ser Leu Pro
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qca tct gta gga gac aga gtc acc atc act tgt agt gca agt cag gac
                                                                   144
Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Gln Asp
         15
att agt aat tat tta aac tgg tat cag cag aaa cca ggg aaa gcc cct
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Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
                         35
aag ctc ctg atc ttt tac tca tca aat tta cac tcg ggg gtc cca tca
Lys Leu Leu Ile Phe Tyr Ser Ser Asn Leu His Ser Gly Val Pro Ser
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agg ttc agc ggc ggt gga tct ggg aca gat tat act ctc acc atc agc Arg Phe Ser Gly Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser 65 70 75	288
agc ctg cag cct gaa gat ttt gca act tat tac tgt cat cag tat agt Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Ser  80 85 90	336
aag ctt ccg tgg acg ttc ggc cag ggg acc aag gta gag att aaa cgt Lys Leu Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg 95 100 105	384
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	_							-	_					gcc Ala		192
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-20
                    -15
ggt acc aga tgt gac atc cag atg acc cag tct cca tcc tcc ctg tct
                                                                   96
Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
             -1
gca tot gta gga gac aga gto acc atc act tgt agt gca agt cag gac
                                                                   144
Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Gln Asp
                                                                   192
att agt aat tat tta aac tgg tat cag cag aaa cca gac aaa gcc gtt
Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Lys Ala Val
                                                                   240
aag ctc ctg atc ttt tac tca tca aat tta cac tcg ggg gtc cca tca
Lys Leu Leu Ile Phe Tyr Ser Ser Asn Leu His Ser Gly Val Pro Ser
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45
agg ttc agc ggc ggt gga tct ggg aca gat tat act ctc acc atc agc
Arg Phe Ser Gly Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser
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agc ctg cag cct gaa gat ttt gca act tat tac tgt cat cag tat agt
                                                                   336
Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Ser
                                 85
             80
                                                                   384
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-20
                    -15
                                        -10
ggt acc aga tgt gac atc cag atg acc cag tct cca tcc tcc ctg tct
Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
             -1
gca tct gta gga gac aga gtc acc atc act tgt agt gca agt cag gac
Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Gln Asp
         15
                             20
att agt aat tat tta aac tgg tat cag cag aaa cca ggg aaa gcc cct
Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
     30
                         35
aaq ctc ctg atc ttt tac tca tca aat tta cac tcg ggg gtc cca tca
Lys Leu Leu Ile Phe Tyr Ser Ser Asn Leu His Ser Gly Val Pro Ser
 45
                     50
                                                                   288
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Arg Phe Ser Gly Gly Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser
aat ctg cag cct gaa gat atc gca act tat tac tgt cat cag tat agt
Asn Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys His Gln Tyr Ser
aag ctt ccg tgg acg ttc ggc cag ggg acc aag gta gag att aaa cgt
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-20
                    -15
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ggt acc aga tgt gac atc cag atg acc cag tct cca tcc tcc ctg tct
Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
             -1
gca tct gta gga gac aga gtc acc atc act tgt agt gca agt cag gac
                                                                   144
Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Gln Asp
         15
att agt aat tat tta aac tgg tat cag cag aaa cca ggg aaa gcc cct
                                                                   192
Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
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                         35
aag ctc ctg atc ttt tac tca tca aat tta cac tcg ggg gtc cca tca
Lys Leu Leu Ile Phe Tyr Ser Ser Asn Leu His Ser Gly Val Pro Ser
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agg ttc agc ggc ggt gga tct ggg aca gat tat act ctc acc atc agc
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Arg Phe Ser Gly Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser
aat ctg cag cct gaa gat ttt gca act tat tac tgt cat cag tat agt
                                                                   336
Asn Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Ser
                                                                   384
aag ctt ccg tgg acg ttc ggc cag ggg acc aag gta gag att aaa cgt
Lys Leu Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
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Met Met Ser Ser Ala Gln Phe Leu Gly Leu Leu Leu Cys Phe Gln
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ggt acc aga tgt gac atc cag atg acc cag tct cca tcc tcc ctg tct
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Gly	Thr	Arg	Cys -1	Asp 1	Ile	Gln	Met	Thr 5	Gln	Ser	Pro	Ser	Ser 10	Leu	Ser	
				gac Asp												144
	_			tta Leu				_	_							192
				ttt Phe												240
				ggt Gly 65												288
_	_	_		gaa Glu	_		_				_		-			336
				acg Thr												384
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ggt acc aga tgt gac atc cag atg acc cag tct gca tcc tcc ctg cct
Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Ser Ala Ser Ser Leu Pro
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gca tct gta gga gac aga gtc acc atc act tgt agt gca agt cag gac
                                                                   144
Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Gln Asp
                             20
         15
att agt aat tat tta aac tgg tat cag cag aaa cca ggg aaa gcc gtt
                                                                   192
Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Val
                         35
                                                                   240
aag ctc ctg atc ttt tac tca tca aat tta cac tcg ggg gtc cca tca
Lys Leu Leu Ile Phe Tyr Ser Ser Asn Leu His Ser Gly Val Pro Ser
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                     50
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						gga Gly											288
	_	_	_		-	gat Asp		_				_		_		_	336
						ttc Phe											384
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						tac Tyr 50											240
						gga Gly											288
	-	_	-		-	gat Asp		-				_					336
	aag	ctt	ccg	tgg	acg	ttc	ggc	cag	ggg	acc	aag	gta	gag	att	aaa	cgt	384

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Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45

Ala Tyr Ile Ser Ser Gly Gly Ser Gly Thr Tyr Tyr Ser Asp Ser Val 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr 65 70 75 80

Leu Gln Met Arg Ser Leu Arg Ala Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Thr Arg Val Lys Leu Gly Thr Tyr Tyr Phe Asp Ser Trp Gly Gln Gly
100 105 110

Thr Leu Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe 115 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu 130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp 145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu 165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser 180 185 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro 195 200 205

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys 210 215 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro 225 230 235 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser 245 250 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp

270 260 265 Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu 310 Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys 325 Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr 345 Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu 395 Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys 410 Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu 450 455 His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr 470 475 Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro 485 Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His 520 525 Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr 555 Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser 565

570

575

Ile Ile Ser Thr Leu Thr 580

<210> 54

<211> 108

<212> PRT

<213> Artificial Sequence

<2205

<223> Description of Artificial Sequence:synthetic protein

<400> 54

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 10 15

Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Lys Ala Val Lys Leu Leu Ile 35 40 45

Phe Tyr Ser Ser Asn Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly 50 55 60

Gly Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro 65 70 75 80

Glu Asp Ile Ala Thr Tyr Phe Cys His Gln Tyr Ser Lys Leu Pro Trp 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg 100 105

<210> 55

<211> 119

<212> PRT

<213> Mus musculus

<400> 55

Glu Val Thr Leu Val Glu Ser Gly Gly Asp Phe Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Lys Val Ser Cys Ala Ala Ser Gly Phe Ala Phe Ser His Tyr 20 25 30

Ala Met Ser Trp Val Arg Gln Thr Pro Ala Lys Arg Leu Glu Trp Val 35 40 45

Ala Tyr Ile Ser Ser Gly Gly Ser Gly Thr Tyr Tyr Ser Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr 65 70 75 80

Leu Gln Met Arg Ser Leu Arg Ser Glu Asp Ser Ala Met Tyr Phe Cys 85 90 95

Thr Arg Val Lys Leu Gly Thr Tyr Tyr Phe Asp Ser Trp Gly Gln Gly
100 105 110

Thr Thr Leu Thr Val Ser Ser 115

<210> 56

<211> 108

<212> PRT

<213> Mus musculus

<400> 56

Asp Ile Gln Met Thr Gln Thr Ala Ser Ser Leu Pro Ala Ser Leu Gly
1 5 10 15

Asp Arg Val Thr Ile Ser Cys Ser Ala Ser Gln Asp Ile Ser Asn Tyr 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile 35 40 45

Phe Tyr Ser Ser Asn Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly 50 60

Gly Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Pro 65 70 75 80

Glu Asp Ile Ala Thr Tyr Phe Cys His Gln Tyr Ser Lys Leu Pro Trp 85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
100 105

<210> 57

<211> 582

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic protein

<400> 57

Glu Val Thr Leu Val Glu Ser Gly Gly Asp Phe Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Lys Val Ser Cys Ala Ala Ser Gly Phe Ala Phe Ser His Tyr

Ala Met Ser Trp Val Arg Gln Thr Pro Ala Lys Arg Leu Glu Trp Val 35 40 45

Ala Tyr Ile Ser Ser Gly Gly Ser Gly Thr Tyr Tyr Ser Asp Ser Val

50 55 60 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu Gln Met Arg Ser Leu Arg Ser Glu Asp Ser Ala Met Tyr Phe Cys Thr Arg Val Lys Leu Gly Thr Tyr Tyr Phe Asp Ser Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu 135 Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp 150 155 Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu 170 Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser 185 Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser 250 245 Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu 305 310 315 Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr



355 360 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu 370 375 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu 385 390 395 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys 405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu 420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
435 440 445

Lys Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu 450 455 460

His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr 465 470 475 480

Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro 485 490 490

Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu 500 505 510

Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His 515 520 525

Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu 530 535 540

Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr 545 550 555 560

Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser 565 570 575

Ile Ile Ser Thr Leu Thr 580